



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/645,085

Source: IPWS

Date Processed by STIC: 11/12/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/645,085
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics _____ Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino _____ Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 _____ "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> _____ Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species) <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 0001/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 _____ "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/645,085

DATE: 11/17/2003
TIME: 15:15:50

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\11172003\J645085.raw

3 <110> APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
W--> 4 <120> TITLE OF INVENTION: Agonist antibody
W--> 5 <130> FILE REFERENCE: FP1009
E--> 6 <140> CURRENT APPLICATION NUMBER: US/10/645,085
C--> 6 <141> CURRENT FILING DATE: 2002-10-07
7 <150> PRIOR APPLICATION NUMBER: JP2000-115246
8 <151> PRIOR FILING DATE: 2000-04-17
9 <150> PRIOR APPLICATION NUMBER: JP2000-321821
10 <151> PRIOR FILING DATE: 2000-10-20
11 <150> PRIOR APPLICATION NUMBER: JP2000-321822
12 <151> PRIOR FILING DATE: 2000-10-20
13 <150> PRIOR APPLICATION NUMBER: PCT/JP01/01912
14 <151> PRIOR FILING DATE: 2001-03-12
E--> 16 <160> NUMBER OF SEQ ID NOS: 109

*PSI: all nucleotides
MUST be in
lower-case letters*

pp 1-5

ERRORED SEQUENCES

1210 <210> SEQ ID NO: 60
1211 <211> LENGTH: 115 / 108 shown below
1212 <212> TYPE: DNA
1213 <213> ORGANISM: Artificial Sequence
W--> 1214 <220> FEATURE:
1215 <223> OTHER INFORMATION: 12B5VH-4
W--> 1216 <400> SEQUENCE: 60
1217 actcgagacg gtgaccattg ttccttggcc ccagatatcg aaaccataat gtcctcctct 60
E--> 1218 cgcacagtaa tacacagcgg tgcctcgggc tctcaggctg ttcatttg 108

1238 <210> SEQ ID NO: 63
1239 <211> LENGTH: 433 / 432 (p.2)
1240 <212> TYPE: DNA
1241 <213> ORGANISM: Human
W--> 1242 <220> FEATURE:
1243 <221> NAME/KEY: CDS
1244 <222> LOCATION: (12)...(419)
1245 <223> OTHER INFORMATION: HEF-12B5H-g gamma. 12-419 peptide

W--> 1246 <400> SEQUENCE: 63
1247 aagcttcac c atg gag ttt ggg ctg agc tgg gtt ttc ctc gtt gct ctt tta aga 56
1248 Met MET Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg
1249 1 5 10 15
1250 ggt gtc cag tgt cag gtg cag ctg gtg cag tct ggg gga ggc ttg gtc cgg ccc ggg ggg 116
1251 Gly Val Gln Cys Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Arg Pro Gly Gly
1252 20 25 30 35
1253 tcc ctg agt ctc tcc tgt gca gtc tct gga alc acc ctc agg acc tac ggc atg cac lgg 176

*Per 1.822 of sequence
Rule, a MAXIMUM of 16
codons per line*

*insert
a hard
return
after 16th
codon*

16 codons MAXIMUM per line (please edit)

1/6 Codons per line only

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/645,085

DATE: 11/17/2003

TIME: 15:15:50

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\11172003\J645085.raw

met

```

1254 Ser Leu Ser Leu Ser Cys Ala Val Ser Gly Ile Thr Leu Arg Thr Tyr Gly MET His Trp
1255                               40                               45                               50                               55
1256 gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg gca ggt ata tcc ttt gac gga aga 236
1257 Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Gly Ile Ser Phe Asp Gly Arg
1258                               60                               65                               70                               75
1259 agt gaa tac tat gca gac tcc gtg cag ggc cga ttc acc atc tcc aga gac agt tcc aag 296
1260 Ser Glu Tyr Tyr Ala Asp Ser Val Gln Gly Arg Phe Thr Ile Ser Arg Asp Ser Ser Lys
1261                               80                               85                               90                               95
1262 aac acc ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 356
1263 Asn Thr Leu Tyr Leu Gln MET Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
1264                               100                              105                              110                              115
1265 gcg aga gga gca cat tat ggt ttc gat atc tgg ggc caa ggg aca atg gtc acc gtc tcg 416
1266 Ala Arg Gly Ala His Tyr Gly Phe Asp Ile Trp Gly Gln Gly Thr MET Val Thr Val Ser
1267                               120                              125                              130                              135

E--> 1268 agt ggtgagtgga tcc 433
E--> 1269 Ser
1271 <210> SEQ ID NO: 64
1272 <211> LENGTH: 323
1273 <212> TYPE: DNA
1274 <213> ORGANISM: Human
W--> 1275 <220> FEATURE:
1276 <221> NAME/KEY: CDS
1277 <222> LOCATION: (1)...(323)
1278 <223> OTHER INFORMATION: 12B5LV. 1-323 peptide
W--> 1279 <400> SEQUENCE: 64
1280 gac atc cag atg acc cag tct cct tcc acc ctg tct gca tct att gga gac aga gtc acc 60
1281 Asp Ile Gln MET Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Ile Gly Asp Arg Val Thr
1282                               5                               10                               15                               20
1283 atc acc tgc cgg gcc agc gag ggt att tat cac tgg ttg gcc tgg tat cag cag aag cca 120
1284 Ile Thr Cys Arg Ala Ser Glu Gly Ile Tyr His Trp Leu Ala Trp Tyr Gln Gln Lys Pro
1285                               25                               30                               35                               40
1286 ggg aaa gcc cct aaa ctc ctg atc tat aag gcc tct agt tta gcc agt ggg gcc cca tca 180
1287 Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu Ala Ser Gly Ala Pro Ser
1288                               45                               50                               55                               60
1289 agg ttc agc ggc agt gga tct ggg aca gat ttc act ctc acc atc agc agc ctg cag cct 240
1290 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1291                               65                               70                               75                               80
1292 gat gat ttt gca act tat tac tgc caa caa tat agt aat tat ccg ctc act ttc ggc gga 300
1293 Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Leu Thr Phe Gly Gly
1294                               85                               90                               95                               100

E--> 1295 ggg acc aag ctg gag atc aaa 323
1296 Gly Thr Lys Leu Glu Ile Lys 321
E--> 1297                               105
1344 <210> SEQ ID NO: 69
1345 <211> LENGTH: 110
1346 <212> TYPE: DNA
1347 <213> ORGANISM: Artificial Sequence
W--> 1348 <220> FEATURE:
1349 <223> OTHER INFORMATION: 12B5VI-4

```

1/6 Codons per line

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/645,085

DATE: 11/17/2003

TIME: 15:15:50

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\11172003\J645085.raw

W--> 1350 <400> SEQUENCE: 69

1351 accatcagca gctgcagcc tgatgatttt gcaacttatt actgccaaca atatagtaat 60

E--> 1352 tatccgctca ctttcggcgg agggaccaag ctggagatca aa

102 ←

Edit all sequences in which
more than 16 codons per line
are shown

see pp 4-5 for more errors

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4

<400> 6

atg	gaa	tgg	agc	tgg	ata	ttt	ctc	ttc	ctc	ctg	tca	gga	act	gca	45
Met	Glu	Trp	Ser	Trp	Ile	Phe	Leu	Phe	Leu	Leu	Ser	Gly	Thr	Ala	
				5					10					15	
ggt	gtc	cac	tcc	cag	gtc	cag	ctg	cag	cag	tct	gga	cct	gac	ctg	90
Gly	Val	His	Ser	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Asp	Leu	
				10	20				25					30	
gta	aag	cct	ggg	gct	tca	gtg	aag	atg	tcc	tgc	aag	gct	tct	gga	135
Val	Lys	Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	
				35					40					45	

10/645,085

5

<210> 72 *last sequence in submitted file*

<211> 415

<212> DNA

<213> Human

<220>

<221> CDS

<222> (12)...(398)

<223> HEF-12B5H-g kappa. 12-398 peptide

<400> 72

aagcttcac c atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc 56

(MET) Asp MET Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu

1

5

10

15

tgg ctc cca ggt gcc aaa tgt gac atc cag atg acc cag tct cct tcc acc ctg tct gca 116

116

(format error)

see item 1 on Error Summary Sheet)

This error appears throughout sequence 72

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 11/17/2003
PATENT APPLICATION: US/10/645,085 TIME: 15:15:51

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\11172003\J645085.raw

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

- Seq#:55; Line(s) 1148,1151,1154,1157,1160
- Seq#:63; Line(s) 1250,1251,1253,1254,1256,1257,1259,1260,1262,1263,1265
- Seq#:63; Line(s) 1266
- Seq#:64; Line(s) 1280,1283,1286,1289,1292
- Seq#:65; Line(s) 1308
- Seq#:72; Line(s) 1384,1385,1387,1388,1390,1391,1393,1394,1396,1397

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/645,085

DATE: 11/17/2003

TIME: 15:15:51

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\11172003\J645085.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:282 E: Numeric Field Identifier Missing, <140> CURRENT APPLICATION NUMBER: is Added.
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:22 M:283 W: Missing Blank Line separator, <220> field identifier
L:24 M:283 W: Missing Blank Line separator, <400> field identifier
L:31 M:283 W: Missing Blank Line separator, <220> field identifier
L:33 M:283 W: Missing Blank Line separator, <400> field identifier
L:40 M:283 W: Missing Blank Line separator, <220> field identifier
L:42 M:283 W: Missing Blank Line separator, <400> field identifier
L:49 M:283 W: Missing Blank Line separator, <220> field identifier
L:51 M:283 W: Missing Blank Line separator, <400> field identifier
L:58 M:283 W: Missing Blank Line separator, <220> field identifier
L:62 M:283 W: Missing Blank Line separator, <400> field identifier
L:95 M:283 W: Missing Blank Line separator, <220> field identifier
L:99 M:283 W: Missing Blank Line separator, <400> field identifier
L:105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:134 M:283 W: Missing Blank Line separator, <220> field identifier
L:138 M:283 W: Missing Blank Line separator, <400> field identifier
L:171 M:283 W: Missing Blank Line separator, <220> field identifier
L:175 M:283 W: Missing Blank Line separator, <400> field identifier
L:210 M:283 W: Missing Blank Line separator, <220> field identifier
L:212 M:283 W: Missing Blank Line separator, <400> field identifier
L:219 M:283 W: Missing Blank Line separator, <220> field identifier
L:221 M:283 W: Missing Blank Line separator, <400> field identifier
L:228 M:283 W: Missing Blank Line separator, <220> field identifier
L:230 M:283 W: Missing Blank Line separator, <400> field identifier
L:237 M:283 W: Missing Blank Line separator, <220> field identifier
L:239 M:283 W: Missing Blank Line separator, <400> field identifier
L:246 M:283 W: Missing Blank Line separator, <220> field identifier
L:248 M:283 W: Missing Blank Line separator, <400> field identifier
L:255 M:283 W: Missing Blank Line separator, <220> field identifier
L:257 M:283 W: Missing Blank Line separator, <400> field identifier
L:264 M:283 W: Missing Blank Line separator, <220> field identifier
L:266 M:283 W: Missing Blank Line separator, <400> field identifier
L:273 M:283 W: Missing Blank Line separator, <220> field identifier
L:275 M:283 W: Missing Blank Line separator, <400> field identifier
L:282 M:283 W: Missing Blank Line separator, <220> field identifier
L:284 M:283 W: Missing Blank Line separator, <400> field identifier
L:291 M:283 W: Missing Blank Line separator, <220> field identifier
L:293 M:283 W: Missing Blank Line separator, <400> field identifier
L:300 M:283 W: Missing Blank Line separator, <220> field identifier
L:302 M:283 W: Missing Blank Line separator, <400> field identifier
L:311 M:283 W: Missing Blank Line separator, <220> field identifier
L:315 M:283 W: Missing Blank Line separator, <400> field identifier
L:377 M:283 W: Missing Blank Line separator, <220> field identifier
L:379 M:283 W: Missing Blank Line separator, <400> field identifier
L:386 M:283 W: Missing Blank Line separator, <220> field identifier

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/645,085

DATE: 11/17/2003

TIME: 15:15:51

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\11172003\J645085.raw

L:388 M:283 W: Missing Blank Line separator, <400> field identifier
L:395 M:283 W: Missing Blank Line separator, <220> field identifier
L:399 M:283 W: Missing Blank Line separator, <400> field identifier
L:442 M:112 C: (48) String data converted to lower case,
L:461 M:283 W: Missing Blank Line separator, <220> field identifier
L:465 M:283 W: Missing Blank Line separator, <400> field identifier
L:1218 M:252 E: No. of Seq. differs, <211> LENGTH:Input:115 Found:108 SEQ:60 ✓
L:1268 M:254 E: No. of Bases conflict, LENGTH:Input:433 Counted:432 SEQ:63 ✓
L:1269 M:252 E: No. of Seq. differs, <211> LENGTH:Input:433 Found:432 SEQ:63 ✓
L:1295 M:254 E: No. of Bases conflict, LENGTH:Input:323 Counted:321 SEQ:64 ✓
L:1297 M:252 E: No. of Seq. differs, <211> LENGTH:Input:323 Found:321 SEQ:64 ✓
L:1311 M:112 C: (48) String data converted to lower case,
L:1352 M:252 E: No. of Seq. differs, <211> LENGTH:Input:110 Found:102 SEQ:69 ✓
L:16 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (109) Counted (72)